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RAW SEQUENCE LISTING

DATE: 05/22/2002

PATENT APPLICATION: US/09/700,906A

TIME: 13:43:29

Input Set : A:\PA32470US seq list.txt

Output Set: N:\CRF3\05222002\I700906A.raw

4 <110> APPLICANT: Forschungszentrum Borstel
 6 <120> TITLE OF INVENTION: Antisense oligonucleotides for treatment of
 7 proliferating cells
 10 <130> FILE REFERENCE: P50303
 12 <140> CURRENT APPLICATION NUMBER: US/09/700,906A
 C--> 13 <141> CURRENT FILING DATE: 2002-04-15
 15 <150> PRIOR APPLICATION NUMBER: DE 198 22 954.2
 16 <151> PRIOR FILING DATE: 1998-05-22
 18 <160> NUMBER OF SEQ ID NOS: 3
 20 <170> SOFTWARE: PatentIn Vers. 2.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 12493
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (197)..(9964)
 31 <400> SEQUENCE: 1
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 34 gacgagcggt ggttcgacaa gtggccttgc gggccggatc gtcccagtg aagagttgta 120
 36 aatttgcttc tggccttccc ctacggatta tacctggcct tcccctacgg attatactca 180
 38 acttactgtt tagaaa atg tgg ccc acg aga cgc ctg gtt act atc aaa agg 232
 39 Met Trp Pro Thr Arg Arg Leu Val Thr Ile Lys Arg
 40 1 5 10
 42 agc ggg gtc gac ggt ccc cac ttt ccc ctg agc ctc agc acc tgc ttg 280
 43 Ser Gly Val Asp Gly Pro His Phe Pro Leu Ser Leu Ser Thr Cys Leu
 44 15 20 25
 46 ttt gga agg ggt att gaa tgt gac atc cgt atc cag ctt cct gtt gtg 328
 47 Phe Gly Arg Gly Ile Glu Cys Asp Ile Arg Ile Gln Leu Pro Val Val
 48 30 35 40
 50 tca aaa caa cat tgc aaa gtt gaa atc cat gag cag gag gca ata tta 376
 51 Ser Lys Gln His Cys Lys Val Glu Ile His Glu Gln Glu Ala Ile Leu
 52 45 50 55 60
 54 cat aat ttc agt tcc aca aat cca aca caa gta aat ggg tct gtt att 424
 55 His Asn Phe Ser Ser Thr Asn Pro Thr Gln Val Asn Gly Ser Val Ile
 56 65 70 75
 58 gat gag cct gta cgg cta aaa cat gga gat gta ata act att att gat 472
 59 Asp Glu Pro Val Arg Leu Lys His Gly Asp Val Ile Thr Ile Ile Asp
 60 80 85 90
 62 cgt tcc ttc agg tat gaa aat gaa agt ctt cag aat gga agg aag tca 520
 63 Arg Ser Phe Arg Tyr Glu Asn Glu Ser Leu Gln Asn Gly Arg Lys Ser
 64 95 100 105
 66 act gaa ttt cca aga aaa ata cgt gaa cag gag cca gca cgt cgt gtc 568

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67 Thr Glu Phe Pro Arg Lys Ile Arg Glu Gln Glu Pro Ala Arg Arg Val
68 110 115 120
70 tca aga tct agc ttc tct tct gac cct gat gag aaa gct caa gat tcc 616
71 Ser Arg Ser Ser Phe Ser Ser Asp Pro Asp Glu Lys Ala Gln Asp Ser
72 125 130 135 140
74 aag gcc tat tca aaa atc act gaa gga aaa gtt tca gga aat cct cag 664
75 Lys Ala Tyr Ser Lys Ile Thr Glu Gly Lys Val Ser Gly Asn Pro Gln
76 145 150 155
78 gta cat atc aag aat gtc aaa gaa gac agt acc gca gat gac tca aaa 712
79 Val His Ile Lys Asn Val Lys Glu Asp Ser Thr Ala Asp Asp Ser Lys
80 160 165 170
82 gac agt gtt gct cag gga aca act aat gtt cat tcc tca gaa cat gct 760
83 Asp Ser Val Ala Gln Gly Thr Thr Asn Val His Ser Ser Glu His Ala
84 175 180 185
86 gga cgt aat ggc aga aat gca gct gat ccc att tct ggg gat ttt aaa 808
87 Gly Arg Asn Gly Arg Asn Ala Ala Asp Pro Ile Ser Gly Asp Phe Lys
88 190 195 200
90 gaa att tcc agc gtt aaa tta gtg agc cgt tat gga gaa ttg aag tct 856
91 Glu Ile Ser Ser Val Lys Leu Val Ser Arg Tyr Gly Glu Leu Lys Ser
92 205 210 215 220
94 gtt ccc act aca caa tgt ctt gac aat agc aaa aaa aat gaa tct ccc 904
95 Val Pro Thr Thr Gln Cys Leu Asp Asn Ser Lys Lys Asn Glu Ser Pro
96 225 230 235
98 ttt tgg aag ctt tat gag tca gtg aag aaa gag ttg gat gta aaa tca 952
99 Phe Trp Lys Leu Tyr Glu Ser Val Lys Lys Glu Leu Asp Val Lys Ser
100 240 245 250
102 caa aaa gaa aat gtc cta cag tat tgt aga aaa tct gga tta caa act 1000
103 Gln Lys Glu Asn Val Leu Gln Tyr Cys Arg Lys Ser Gly Leu Gln Thr
104 255 260 265
106 gat tac gca aca gag aaa gaa agt gct gat ggt tta cag ggg gag acc 1048
107 Asp Tyr Ala Thr Glu Lys Glu Ser Ala Asp Gly Leu Gln Gly Glu Thr
108 270 275 280
110 caa ctg ttg gtc tcg cgt aag tca aga cca aaa tct ggt ggg agc ggc 1096
111 Gln Leu Leu Val Ser Arg Lys Ser Arg Pro Lys Ser Gly Gly Ser Gly
112 285 290 295 300
114 cac gct gtg gca gag cct gct tca cct gaa caa gag ctt gac cag aac 1144
115 His Ala Val Ala Glu Pro Ala Ser Pro Glu Gln Glu Leu Asp Gln Asn
116 305 310 315
118 aag ggg aag gga aga gac gtg gag tct gtt cag act ccc agc aag gct 1192
119 Lys Gly Lys Gly Arg Asp Val Glu Ser Val Gln Thr Pro Ser Lys Ala
120 320 325 330
122 gtg ggc gcc agc ttt cct ctc tat gag ccg gct aaa atg aag acc cct 1240
123 Val Gly Ala Ser Phe Pro Leu Tyr Glu Pro Ala Lys Met Lys Thr Pro
124 335 340 345
126 gta caa tat tca cag caa caa aat tct cca caa aaa cat aag aac aaa 1288
127 Val Gln Tyr Ser Gln Gln Gln Asn Ser Pro Gln Lys His Lys Asn Lys
128 350 355 360
130 gac ctg tat act act ggt aga aga gaa tct gtg aat ctg ggt aaa agt 1336
131 Asp Leu Tyr Thr Thr Gly Arg Arg Glu Ser Val Asn Leu Gly Lys Ser

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132	365		370		375		380	
134	gaa ggc ttc aag gct ggt gat aaa act ctt act ccc agg aag ctt tca	1384						
135	Glu Gly Phe Lys Ala Gly Asp Lys Thr Leu Thr Pro Arg Lys Leu Ser							
136			385		390		395	
138	act aga aat cga aca cca gct aaa gtt gaa gat gca gct gac tct gcc	1432						
139	Thr Arg Asn Arg Thr Pro Ala Lys Val Glu Asp Ala Ala Asp Ser Ala							
140			400		405		410	
142	act aag cca gaa aat ctc tct tcc aaa acc aga gga agt att cct aca	1480						
143	Thr Lys Pro Glu Asn Leu Ser Ser Lys Thr Arg Gly Ser Ile Pro Thr							
144			415		420		425	
146	gat gtg gaa gtt ctg cct acg gaa act gaa att cac aat gag cca ttt	1528						
147	Asp Val Glu Val Leu Pro Thr Glu Thr Glu Ile His Asn Glu Pro Phe							
148			430		435		440	
150	tta act ctg tgg ctc act caa gtt gag agg aag atc caa aag gat tcc	1576						
151	Leu Thr Leu Trp Leu Thr Gln Val Glu Arg Lys Ile Gln Lys Asp Ser							
152	445		450		455		460	
154	ctc agc aag cct gag aaa ttg ggc act aca gct gga cag atg tgc tct	1624						
155	Leu Ser Lys Pro Glu Lys Leu Gly Thr Thr Ala Gly Gln Met Cys Ser							
156			465		470		475	
158	ggg tta cct ggt ctt agt tca gtt gat atc aac aac ttt ggt gat tcc	1672						
159	Gly Leu Pro Gly Leu Ser Ser Val Asp Ile Asn Asn Phe Gly Asp Ser							
160			480		485		490	
162	att aat gag agt gag gga ata cct ttg aaa aga agg cgt gtg tcc ttt	1720						
163	Ile Asn Glu Ser Glu Gly Ile Pro Leu Lys Arg Arg Val Ser Phe							
164			495		500		505	
166	ggt ggg cac cta aga cct gaa cta ttt gat gaa aac ttg cct cct aat	1768						
167	Gly Gly His Leu Arg Pro Glu Leu Phe Asp Glu Asn Leu Pro Pro Asn							
168			510		515		520	
170	acg cct ctc aaa agg gga gaa gcc cca acc aaa aga aag tct ctg gta	1816						
171	Thr Pro Leu Lys Arg Gly Glu Ala Pro Thr Lys Arg Lys Ser Leu Val							
172	525		530		535		540	
174	atg cac act cca cct gtc ctg aag aaa atc atc aag gaa cag cct caa	1864						
175	Met His Thr Pro Pro Val Leu Lys Lys Ile Ile Lys Glu Gln Pro Gln							
176			545		550		555	
178	cca tca gga aaa caa gag tca ggt tca gaa atc cat gtg gaa gtg aag	1912						
179	Pro Ser Gly Lys Gln Glu Ser Gly Ser Glu Ile His Val Glu Val Lys							
180			560		565		570	
182	gca caa agc ttg gtt ata agc cct cca gct cct agt cct agg aaa act	1960						
183	Ala Gln Ser Leu Val Ile Ser Pro Pro Ala Pro Ser Pro Arg Lys Thr							
184			575		580		585	
186	cca gtt gcc agt gat caa cgc cgt agg tcc tgc aaa aca gcc cct gct	2008						
187	Pro Val Ala Ser Asp Gln Arg Arg Ser Cys Lys Thr Ala Pro Ala							
188			590		595		600	
190	tcc agc agc aaa tct cag aca gag gtt cct aag aga gga gga gaa aga	2056						
191	Ser Ser Ser Lys Ser Gln Thr Glu Val Pro Lys Arg Gly Gly Glu Arg							
192	605		610		615		620	
194	gtg gca acc tgc ctt caa aag aga gtg tct atc agc cga agt caa cat	2104						
195	Val Ala Thr Cys Leu Gln Lys Arg Val Ser Ile Ser Arg Ser Gln His							
196			625		630		635	

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198 gat att tta cag atg ata tgt tcc aaa aga aga agt ggt gct tcg gaa 2152
199 Asp Ile Leu Gln Met Ile Cys Ser Lys Arg Arg Ser Gly Ala Ser Glu
200 640 645 650
202 gca aat ctg att gtt gca aaa tca tgg gca gat gta gta aaa ctt ggt 2200
203 Ala Asn Leu Ile Val Ala Lys Ser Trp Ala Asp Val Val Lys Leu Gly
204 655 660 665
206 gca aaa caa aca caa act aaa gtc ata aaa cat ggt cct caa agg tca 2248
207 Ala Lys Gln Thr Gln Thr Lys Val Ile Lys His Gly Pro Gln Arg Ser
208 670 675 680
210 atg aac aaa agg caa aga aga cct gct act cca aag aag cct gtg ggc 2296
211 Met Asn Lys Arg Gln Arg Arg Pro Ala Thr Pro Lys Lys Pro Val Gly
212 685 690 695 700
214 gaa gtt cac agt caa ttt agt aca ggc cac gca aac tct cct tgt acc 2344
215 Glu Val His Ser Gln Phe Ser Thr Gly His Ala Asn Ser Pro Cys Thr
216 705 710 715
218 ata ata ata ggg aaa gct cat act gaa aaa gta cat gtg cct gct cga 2392
219 Ile Ile Ile Gly Lys Ala His Thr Glu Lys Val His Val Pro Ala Arg
220 720 725 730
222 ccc tac aga gtg ctc aac aac ttc att tcc aac caa aaa atg gac ttt 2440
223 Pro Tyr Arg Val Leu Asn Asn Phe Ile Ser Asn Gln Lys Met Asp Phe
224 735 740 745
226 aag gaa gat ctt tca gga ata gct gaa atg ttc aag acc cca gtg aag 2488
227 Lys Glu Asp Leu Ser Gly Ile Ala Glu Met Phe Lys Thr Pro Val Lys
228 750 755 760
230 gag caa ccg cag ttg aca agc aca tgt cac atc gct att tca aat tca 2536
231 Glu Gln Pro Gln Leu Thr Ser Thr Cys His Ile Ala Ile Ser Asn Ser
232 765 770 775 780
234 gag aat ttg ctt gga aaa cag ttt caa gga act gat tca gga gaa gaa 2584
235 Glu Asn Leu Leu Gly Lys Gln Phe Gln Gly Thr Asp Ser Gly Glu Glu
236 785 790 795
238 cct ctg ctc ccc acc tca gag agt ttt gga gga aat gtg ttc ttc agt 2632
239 Pro Leu Leu Pro Thr Ser Glu Ser Phe Gly Gly Asn Val Phe Phe Ser
240 800 805 810
242 gca cag aat gca gca aaa cag cca tct gat aaa tgc tct gca agc cct 2680
243 Ala Gln Asn Ala Ala Lys Gln Pro Ser Asp Lys Cys Ser Ala Ser Pro
244 815 820 825
246 ccc tta aga cgg cag tgt att aga gaa aat gga aac gta gca aaa acg 2728
247 Pro Leu Arg Arg Gln Cys Ile Arg Glu Asn Gly Asn Val Ala Lys Thr
248 830 835 840
250 ccc agg aac acc tac aaa atg act tct ctg gag aca aaa act tca gat 2776
251 Pro Arg Asn Thr Tyr Lys Met Thr Ser Leu Glu Thr Lys Thr Ser Asp
252 845 850 855 860
254 act gag aca gag cct tca aaa aca gta tcc act gta aac agg tca gga 2824
255 Thr Glu Thr Glu Pro Ser Lys Thr Val Ser Thr Val Asn Arg Ser Gly
256 865 870 875
258 agg tct aca gag ttc agg aat ata cag aag cta cct gtg gaa agt aag 2872
259 Arg Ser Thr Glu Phe Arg Asn Ile Gln Lys Leu Pro Val Glu Ser Lys
260 880 885 890
262 agt gaa gaa aca aat aca gaa att gtt gag tgc atc cta aaa aga ggt 2920

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266	cag	aag	gca	aca	cta	cta	caa	caa	agg	aga	gaa	gga	gag	atg	aag	gaa	2968
267	Gln	Lys	Ala	Thr	Leu	Leu	Gln	Gln	Arg	Arg	Glu	Gly	Glu	Met	Lys	Glu	
268		910						915					920				
270	ata	gaa	aga	cct	ttt	gag	aca	tat	aag	gaa	aat	att	gaa	tta	aaa	gaa	3016
271	Ile	Glu	Arg	Pro	Phe	Glu	Thr	Tyr	Lys	Glu	Asn	Ile	Glu	Leu	Lys	Glu	
272	925						930					935				940	
274	aac	gat	gaa	aag	atg	aaa	gca	atg	aag	aga	tca	aga	act	tgg	ggg	cag	3064
275	Asn	Asp	Glu	Lys	Met	Lys	Ala	Met	Lys	Arg	Ser	Arg	Thr	Trp	Gly	Gln	
276					945					950					955		
278	aaa	tgt	gca	cca	atg	tct	gac	ctg	aca	gac	ctc	aag	agc	ttg	cct	gat	3112
279	Lys	Cys	Ala	Pro	Met	Ser	Asp	Leu	Thr	Asp	Leu	Lys	Ser	Leu	Pro	Asp	
280					960					965					970		
282	aca	gaa	ctc	atg	aaa	gac	acg	gca	cgt	ggc	cag	aat	ctc	ctc	caa	acc	3160
283	Thr	Glu	Leu	Met	Lys	Asp	Thr	Ala	Arg	Gly	Gln	Asn	Leu	Leu	Gln	Thr	
284					975					980					985		
286	caa	gat	cat	gcc	aag	gca	cca	aag	agt	gag	aaa	ggc	aaa	atc	act	aaa	3208
287	Gln	Asp	His	Ala	Lys	Ala	Pro	Lys	Ser	Glu	Lys	Gly	Lys	Ile	Thr	Lys	
288		990					995					1000					
290	atg	ccc	tgc	cag	tca	tta	caa	cca	gaa	cca	ata	aac	acc	cca	aca	cac	3256
291	Met	Pro	Cys	Gln	Ser	Leu	Gln	Pro	Glu	Pro	Ile	Asn	Thr	Pro	Thr	His	
292	1005					1010						1015				1020	
294	aca	aaa	caa	cag	ttg	aag	gca	tcc	ctg	ggg	aaa	gta	ggt	gtg	aaa	gaa	3304
295	Thr	Lys	Gln	Gln	Leu	Lys	Ala	Ser	Leu	Gly	Lys	Val	Gly	Val	Lys	Glu	
296					1025					1030					1035		
298	gag	ctc	cta	gca	gtc	ggc	aag	ttc	aca	cgg	acg	tca	ggg	gag	acc	acg	3352
299	Glu	Leu	Leu	Ala	Val	Gly	Lys	Phe	Thr	Arg	Thr	Ser	Gly	Glu	Thr	Thr	
300					1040					1045					1050		
302	cac	acg	cac	aga	gag	cca	gca	gga	gat	ggc	aag	agc	atc	aga	acg	ttt	3400
303	His	Thr	His	Arg	Glu	Pro	Ala	Gly	Asp	Gly	Lys	Ser	Ile	Arg	Thr	Phe	
304					1055					1060					1065		
306	aag	gag	tct	cca	aag	cag	atc	ctg	gac	cca	gca	gcc	cgt	gta	act	gga	3448
307	Lys	Glu	Ser	Pro	Lys	Gln	Ile	Leu	Asp	Pro	Ala	Ala	Arg	Val	Thr	Gly	
308		1070					1075					1080					
310	atg	aag	aag	tgg	cca	aga	acg	cct	aag	gaa	gag	gcc	cag	tca	cta	gaa	3496
311	Met	Lys	Lys	Trp	Pro	Arg	Thr	Pro	Lys	Glu	Glu	Ala	Gln	Ser	Leu	Glu	
312	1085					1090						1095				1100	
314	gac	ctg	gct	ggc	ttc	aaa	gag	ctc	ttc	cag	aca	cca	ggt	ccc	tct	gag	3544
315	Asp	Leu	Ala	Gly	Phe	Lys	Glu	Leu	Phe	Gln	Thr	Pro	Gly	Pro	Ser	Glu	
316					1105					1110					1115		
318	gaa	tca	atg	act	gat	gag	aaa	act	acc	aaa	ata	gcc	tgc	aaa	tct	cca	3592
319	Glu	Ser	Met	Thr	Asp	Glu	Lys	Thr	Thr	Lys	Ile	Ala	Cys	Lys	Ser	Pro	
320					1120					1125					1130		
322	cca	cca	gaa	tca	gtg	gac	act	cca	aca	agc	aca	aag	caa	tgg	cct	aag	3640
323	Pro	Pro	Glu	Ser	Val	Asp	Thr	Pro	Thr	Ser	Thr	Lys	Gln	Trp	Pro	Lys	
324					1135					1140					1145		
326	aga	agt	ctc	agg	aaa	gca	gat	gta	gag	gaa	gaa	ttc	tta	gca	ctc	agg	3688
327	Arg	Ser	Leu	Arg	Lys	Ala	Asp	Val	Glu	Glu	Glu	Phe	Leu	Ala	Leu	Arg	

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L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date